

SEQUENCE LISTING

<110> Holloway, James L.
Lok, Si

<120> SECRETED PROTEIN ZACRP4

<130> 99-29

<150> 60/141,928

<151> 1999-07-01

<160> 9

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1357

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210)...(1196)

<400> 1

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ggagcccccg ccgcccctgc cgcagcgcg gcggtcagcg cgcagcccgg caccgcagc      120
ctgcagcctg cagcccgcag cccgcagccc ggagccagat cgcgggctca gaccgaaccc      180
gactcgaccg ccgccccag ccaggcgcc atg ctg ccg ctt ctg ctg ggc ctg      233
                               Met Leu Pro Leu Leu Leu Gly Leu
                               1                               5

ctg ggc cca gcg gcc tgc tgg gcc ctg ggc ccg acc ccc ggc ccg gga      281
Leu Gly Pro Ala Ala Cys Trp Ala Leu Gly Pro Thr Pro Gly Pro Gly
   10                               15                               20

tcc tct gag ctg cgc tcg gcc ttc tcg gcg gca cgc acc acc ccc ctg      329
Ser Ser Glu Leu Arg Ser Ala Phe Ser Ala Ala Arg Thr Thr Pro Leu
   25                               30                               35                               40

gag ggc acg tcg gag atg gcg gtg acc ttc gac aag gtg tac gtg aac      377
Glu Gly Thr Ser Glu Met Ala Val Thr Phe Asp Lys Val Tyr Val Asn

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20250729T090400

55

gcg gcc ggc gtg ttc cgc tgc cgt ctg ccc ggc gcc tac ttc ttc tcc 905
Ala Ala Gly Val Phe Arg Cys Arg Leu Pro Gly Ala Tyr Phe Phe Ser
220 225 230

ttc acg ctg ggc aag ctg ccg cgt aag acg ctg tcg gtt aag ctg atg 953
 Phe Thr Leu Gly Lys Leu Pro Arg Lys Thr Leu Ser Val Lys Leu Met
 235 240 245

aag aac cgc gac gag gtg cag gcc atg att tac gac gac ggc gcg tcg 1001
 Lys Asn Arg Asp Glu Val Gln Ala Met Ile Tyr Asp Asp Gly Ala Ser
 250 255 260

cgg cgc cgc gag atg cag agc cag agc gtg atg ctg gcc ctg cgg cgc 1049
 Arg Arg Arg Glu Met Gln Ser Gln Ser Val Met Leu Ala Leu Arg Arg
 265 270 275 280

ggc gac gcc gtc tgg ctg ctc agc cac gac cac gac ggc tac ggc gcc 1097
 Gly Asp Ala Val Trp Leu Leu Ser His Asp His Asp Gly Tyr Gly Ala
 285 290 295

tac agc aac cac ggc aag tac atc acc ttc tcc ggc ttc ctg gtg tac 1145
 Tyr Ser Asn His Gly Lys Tyr Ile Thr Phe Ser Gly Phe Leu Val Tyr
 300 305 310

ccc gac ctc gcc ccc gcc gcc ccg ccg ggc ctc ggg gcc tcg gag cta 1193
 Pro Asp Leu Ala Pro Ala Ala Pro Pro Gly Leu Gly Ala Ser Glu Leu
 315 320 325

ctg tgagccccgg gccagagaag agccccgggag ggccaggggc gtgcatgcc 1246
 Leu

ggccggggccc gaggtctgaa agtcccgcgc gagcgccacg gcctccgggc gcgcctggac 1306
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<210> 2

<211> 329

<212> PRT

<213> Homo sapiens

<400> 2

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 Leu Gly Pro Thr Pro Gly Pro Gly Ser Ser Glu Leu Arg Ser Ala Phe
 20 25 30
 Ser Ala Ala Arg Thr Thr Pro Leu Glu Gly Thr Ser Glu Met Ala Val
 35 40 45
 Thr Phe Asp Lys Val Tyr Val Asn Ile Gly Gly Asp Phe Asp Val Ala
 50 55 60

40516 4500

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<210> 3
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> C1q Aromatic Motif

<221> VARIANT
<222> (2)...(6)
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<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (7)...(7)

<223> Xaa is asparagine or aspartic acid

<221> VARIANT

<222> (8)...(11)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (12)...(12)

<223> Xaa is phenylalanine, tyrosine, tryptophan or leucine

<221> VARIANT

<222> (13)...(18)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (20)...(24)

<223> Each Xaa is independently any amino acid residue

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<222> (26)...(26)

<223> Xaa is any amino acid residue

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<222> (28)...(28)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (30)...(30)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (31)...(31)

<223> Xaa is phenylalanine or tyrosine

<400> 3

Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
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Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Tyr	Xaa	Phe	Xaa	Xaa		
			20					25							30	

100516-0001

<210> 4
 <211> 987
 <212> DNA
 <213> Artificial Sequence

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<223> Degenerate nucleotide sequence encoding the
 polypeptide of SEQ ID NO:2

<221> variation

<222> (1)...(987)

<223> Each N is A, T, G or C

<400> 4

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garggnacnw	sngaratggc	ngtnacntty	gayaargtnt	aygtnaayat	hggnggngay	180
ttygaygtng	cnacnggnca	rttymgntgy	mgngtnccng	gngcntaytt	yttysntty	240
acngcnggna	argcnccnca	yaarwsnytn	wsngtnatgy	tngtnmgnaa	ymgngaygar	300
gtncargcny	tngcnttyga	ygarcarcarmgn	mgncnggng	cnmgnmgngc	ngcnwsncar	360
wsngcnatgy	tnrcarytnga	ytayggngay	acngtntggy	tnmgnytnca	yggngcncn	420
caytaygcny	tnggngcnc	nggngcnacn	ttywsnggnt	ayytngtnta	ygcngaygc	480
gaygcngayg	cnccngcnmg	nggnccncn	gcncncncng	arccnmgnws	ngcnttywsn	540
gcngcnmgna	cnmgnwsnyt	ngtnggnwsn	gaygcnggnc	cnggnccnmg	ncaycarccn	600
ytngcnttyg	ayacngartt	ygtnaayath	ggnggngayt	tygaygcngc	ngcnggngtn	660
ttymgntgym	gnytnccngg	ngcntaytty	ttywsnttya	cnytnngnaa	rytnccnmgn	720
aaracnytnw	sngtnaaryt	natgaaraay	mgngaygarg	tnrcargcnat	gathtaygay	780
gayggngcnw	snmgnmgnmg	ngaratgcar	wsncarwsng	tnatgytngc	nytnmgnmgn	840
ggngaygcng	tnnggytnyt	nwsncaygay	caygayggnt	ayggngcnta	ywsnaaycay	900
ggnaartaya	thacnttyws	nggnttyytn	gtntayccng	ayytngcncc	ngcngcncn	960
ccnggnytn	gngcnwsnga	rytnytn				987

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Oligonucleotide ZC20,839

<400> 5

atgtacttgc cgtggttgct gtag

24

<210> 6

400645 0220

<211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC20840

<400> 6
 cgacaccgag ttcgtcaaca ttg 23

<210> 7
 <211> 325
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate nucleotide sequence encoding the
 polypeptide of SEQ ID NO:2.

<221> variation
 <222> (1)...(325)
 <223> Each N is independently A, T, C or G.

<400> 7
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 ncttcacgct gggcaagctg ccgcgtaaga cgctgtcggg taagctgatg aagaaccgcg 180
 acgaggtgca ggccatgatt tacgacgacg gcgcgtcgcg gcgccgcgag atgcagagcc 240
 agagcgtgat gctggccctg cggcgcgng acgccgtctg gctgtcagcc acgaccacga 300
 cggctacggc gcctacagca accac 325

<210> 8
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC22162

<400> 8
 ccgcggcacc aaccactc 18

<210> 9
 <211> 18

10005167.000000

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC 22168

<400> 9

gtcgcggttc ttcattcag

18

20/200 4975000

1005457.022702

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C1q 2 FDTEFVNIGGDFDAAAGVERCRLPGAYFFSFTLGKLPRKTLVKLMKNRDEVQAMIYDDG

C1q 1 RRPGARRAASQSAMLQLDYGDTVWL
:. : : : : : : : : :
C1q 2 ASR-RREMQSQSVMLALRRGDAVWL

Figure